

CRF Error Corrected by the STIC Systems Branch

Serial Number: 101020,513

CRF Processing Date: 12/26/02 018
 Edited by: DC #4 2570
 Verified by: DC (STIC staff) 1218

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form. 3/1/95



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/020,513

DATE: 12/26/2002

TIME: 09:16:25

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF4\12262002\J020513.raw

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3 <110> APPLICANT: Degussa AG
5 <120> TITLE OF INVENTION: Nucleotide sequences which code for the ilvE gene
7 <130> FILE REFERENCE: 000759 BT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/020,513
C--> 10 <141> CURRENT FILING DATE: 2002-11-27
12 <160> NUMBER OF SEQ ID NOS: 2
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1453
18 <212> TYPE: DNA
19 <213> ORGANISM: Corynebacterium glutamicum
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (221)..(1321)
24 <223> OTHER INFORMATION: ilvE gene
26 <400> SEQUENCE: 1
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29 tgaagttgtg tctccgcttt ggttggggga ggcatacaat tgaaactaac ttttaacaag 120
31 cctagccatt cctcaaaacc gtgagacgaa attggctatt catcccataa aatggggctg 180
33 actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag 235
34                                     Met Thr Ser Leu Glu
35                                     1           5
37 ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 283
38 Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys
39          10          15          20
41 gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 331
42 Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met
43          25          30          35
45 gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 379
46 Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu
47          40          45          50
49 gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 427
50 Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His
51          55          60          65
53 tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 475
54 Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp
55 70          75          80          85
57 gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag 523
58 Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln
59          90          95          100
60 cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt 571
61 Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe
62          105          110          115

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64 att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct 619
65 Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro
66      120      125      130
68 gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc 667
69 Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser
70      135      140      145
72 acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg 715
73 Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu
74 150      155      160      165
76 gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct 763
77 Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro
78      170      175      180
80 gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga 811
81 Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly
82      185      190      195
84 act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc 859
85 Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala
86      200      205      210
88 cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat 907
89 Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp
90      215      220      225
92 gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg 955
93 Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly
94 230      235      240      245
96 ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt 1003
97 Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu
98      250      255      260
100 tcc ggc tca cta ctt cca ggc atc acc gcg aag tca ctt cta caa gta 1051
101 Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val
102      265      270      275
104 gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc 1099
105 Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr
106      280      285      290
108 gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct 1147
109 Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala
110      295      300      305
112 tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct 1195
113 Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala
114 310      315      320      325
116 cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg 1243
117 His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met
118      330      335      340
120 aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac 1291
121 Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp
122      345      350      355
124 caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga 1341
125 Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
126      360      365
128 ccccgctgca ttaaaccctg atttattgca gcgggggtttt tgcgttgaca agctcttatg 1401

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RAW SEQUENCE LISTING

DATE: 12/26/2002

PATENT APPLICATION: US/10/020,513

TIME: 09:16:25

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF4\12262002\J020513.raw

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130 agacgtaggg ggtggaagca ggggtagggac gtgtccagcc caagtggcat gc      1453
133 <210> SEQ ID NO: 2
134 <211> LENGTH: 367
135 <212> TYPE: PRT
136 <213> ORGANISM: Corynebacterium glutamicum
138 <400> SEQUENCE: 2
139 Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser
140   1           5           10           15
142 Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
143           20           25           30
145 Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
146           35           40           45
148 His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
149           50           55           60
151 Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
152   65           70           75           80
154 Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
155           85           90           95
157 Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
158           100          105          110
160 Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
161           115          120          125
163 Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
164           130          135          140
166 Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
167 145           150          155          160
169 Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
170           165          170          175
172 Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
173           180          185          190
175 Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
176           195          200          205
178 Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
179           210          215          220
181 Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly
182 225           230          235          240
184 Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu
185           245          250          255
187 Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
188           260          265          270
190 Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
191           275          280          285
193 Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
194           290          295          300
196 Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
197 305           310          315          320
199 Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
200           325          330          335
202 Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln

```

DATE: 12/26/2002

TIME: 09:16:26

Output Set: N:\CRF4\12262002\J020513.raw

203 340 345 350
205 Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
206 355 360 365

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/020,513

DATE: 12/26/2002

TIME: 09:16:27

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF4\12262002\J020513.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date



OIPE

Does it Comply
Correctly No Needed

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/020,513

DATE: 12/16/2002

TIME: 13:34:23

Input Set : A:\000759_englisch.app

Output Set: N:\CRF4\12162002\J020513.raw

3 <110> APPLICANT: Degussa AG
 5 <120> TITLE OF INVENTION: Nucleotide sequences which code for the ilvE gene
 7 <130> FILE REFERENCE: 000759 BT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/020,513
 C--> 10 <141> CURRENT FILING DATE: 2002-11-27
 12 <160> NUMBER OF SEQ ID NOS: 2
 14 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

133 <210> SEQ ID NO: 2
 134 <211> LENGTH: 367
 135 <212> TYPE: PRT
 136 <213> ORGANISM: Corynebacterium glutamicum
 138 <400> SEQUENCE: 2
 139 Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser
 140 1 5 10 15
 142 Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
 143 20 25 30
 145 Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 146 35 40 45
 148 His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 149 50 55 60
 151 Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 152 65 70 75 80
 154 Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 155 85 90 95
 157 Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 158 100 105 110
 160 Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 161 115 120 125
 163 Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 164 130 135 140
 166 Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 167 145 150 155 160
 169 Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 170 165 170 175
 172 Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 173 180 185 190
 175 Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 176 195 200 205
 178 Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln

RAW SEQUENCE LISTING

DATE: 12/16/2002

PATENT APPLICATION: US/10/020,513

TIME: 13:34:23

Input Set : A:\000759_englisch.app

Output Set: N:\CRF4\12162002\J020513.raw

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179      210      215      220
181 Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly
182 225      230      235      240
184 Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu
185      245      250      255
187 Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
188      260      265      270
190 Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
191      275      280      285
193 Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
194      290      295      300
196 Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
197 305      310      315      320
199 Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
200      325      330      335
202 Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
203      340      345      350
205 Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
206      355      360      365

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E--> 213 Degussa Aktiengesellschaft Fehler! Textmarke nicht definiert.
E--> 214 60311 Frankfurt

-delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/020,513

DATE: 12/16/2002

TIME: 13:34:24

Input Set : A:\000759_englisch.app

Output Set: N:\CRF4\12162002\J020513.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:213 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:213 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:6
L:214 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:214 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:214 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:214 M:252 E: No. of Seq. differs, <211> LENGTH:Input:367 Found:374 SEQ:2